Instrumental Analysis and Quantitation of Polycyclic Aromatic Hydrocarbons and Atrazine:

IADN Project

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1.0 Introduction

This document briefly outlines the instrumental analysis and quantitation of polycyclic aromatic hydrocarbons (PAH) and atrazine collected in air and precipitation samples from three sites on the Great Lakes. This work is conducted at the School of Public and Environmental Affairs, Indiana University-Bloomington as a part of the Integrated Atmospheric Deposition Network (IADN). The following summarizes the gas chromatographic-mass spectrometry (GC-MS) technique used, its pertinent parameters, and analyte quantitation.

PAH analyses are performed on a Hewlett-Packard (HP) 5890 Series II gas chromatograph and a HP 5989 mass spectrometer. Chromatographic resolution is achieved with a 30 m \times 250 μ m DB-5 capillary column which has a 0.25 μ m film thickness (J & W Scientific, Folsom, CA) with helium carrier gas. PAHs are quantified by GC-MS using selected ion monitoring (SIM) and the method of internal standards. The PAHs analyzed in this study are listed in Table 1 along with the primary and secondary ions from their mass spectra.

Table 1. Target compounds and their monitored ions.

Retention Order	Compound	Major Ion	Secondary Ion
1	d10-anthracene*	188	
2	acenaphthylene	152	151
3	acenaphthene	153	154
4	fluorene	166	165
5	d10-phenanthrene**	188	
6	phenanthrene	178	176
7	anthracene	178	176
8	fluoranthene	202	101
9	pyrene	202	101
10	retene	219	234
11	d12-benzo (a) anthracene*	240	
12	benzo (a) anthracene	228	114
13	chrysene	228	114
14	d12-perylene*	264	
15	benzo (b) fluoranthene	252	126
16	benzo (k) fluoranthene	252	126
17	benzo (e) pyrene	252	126
18	benzo (a) pyrene	252	126
19	indeno (1,2,3,cd) pyrene	276	138

Retention Order	Compound	Major Ion	Secondary Ion
20	dibenzo (a,h) anthracene	278	139
21	benzo (g,h,i) perylene	276	138
22	coronene	300	150

Table 1. Target compounds and their monitored ions.

2.0 Performance Evaluation

Prior to analyzing a sample set, the GC-MS system performance and calibration are verified for all analytes. The mass spectrometer is tuned immediately before the running of a sample batch using the system's operating software programs (AUTOTUNE) with perfluorotributylamine (PFTBA) calibration gas. Mass spectrometer parameters are adjusted so that masses 69, 219, and 502 and their respective isotopes meet the target mass-intensity criteria. A sample AUTOTUNE report is included.

Hexane is injected prior to the running of a sample set to insure the system is free from contaminants or interfering peaks. The Relative Percent Difference (RPD) between a calibration standard and a performance standard should be withing 20%.

Sample injections and system maintenance are recorded in the appropriate laboratory logbooks located near the instrument.

3.0 Instrumental Parameters

The GC oven temperature program is given in Table 2. Other significant gas chromatographic parameters are:

Carrier gas: helium (99.999%; Liquid Carbonic, Chicago)

Injector: On Column, Constant Flow

Injection volume: $1 \mu L$ Transfer line: $300 \,^{\circ} C$

The mass spectrometer is operated in the electron ionization (EI) mode with ion source and quadrapole temperatures of 250° C and 100° C respectively.

^{*}internal standard

^{**}surrogate standard

Table 2. GC oven temperature program for PAH analysis

Initial Temperature: 40°C

Initial Time: 3.00 min

Rate (°C/min)	Final Temperature (°C)	Final Hold Time (min)
30.0	240	0.00
50.0	300	11.7

Total Run Time: 22.70 min

4.0 Sample Analysis

The extracted samples, lab blanks and matrix spikes are stored in 4-mL amber vials at -20 $^{\circ}$ C until they are ready for analysis. They contain approximately 1 mL of solvent (hexane) and were previously spiked with 50 μ L of the internal standard solution (see Table 3).

Table 3. Internal standard solution.

Compound	Concentration (ng/µL)
d10-anthracene	4.00
d12-benzo(a)anthracene	4.00
d12-perylene	4.00

Standards and samples are brought to room temperature before they are injected. After the hexane blank is injected, a calibration standard (see Table 5) is injected followed by the samples. All injections are performed manually with 1 μ L volumes.

The mass spectrometer is turned on after a four minute solvent delay. Data is acquired in selected ion mode. Windows and ion ranges are given in Table 6.

5.0 Data Reduction and Analyte Quantitation

Data is collected and stored within the system's HP Apollo 400 computer. Mass chromatograms are generated, and their peaks are integrated with the accompanying software programs. Chemstation Enviroquant prepares quantitation reports with individual mass chromatograms and spectra for all target analytes.

For each day of samples run, relative response factors (RRFs) for each analyte are determined from the calibration standard's peak areas using Equation 1.

$$RRF_{std} = \left(\frac{mass_a}{area_a}\right)_{std} \div \left(\frac{mass_{istd}}{area_{istd}}\right)_{std}$$

Where $mass_a = the$ analyte's known mass in the injected amount of calibration standard, $area_a = the$ analyte's peak area, $mass_{istd} = the$ known mass of the appropriate internal standard, and $area_{istd} = that$ internal standard's peak area.

With reference to Table 1, the response factors for compounds 2-10, 12-13, and 15-22 are calculated relative to the internal standards d10-anthracene, d12-benzo(a)anthracene, and d12-perylene respectively.

An analyte's mass in a sample ($mass_a$) is calculated from the RRF_{std} above and the internal standard response in the sample by the following equation:

$$(mass_a)_{sample} = (area_a)_{sample} \times RRF_{std} \times \left(\frac{mass_{istd}}{area_{istd}}\right)_{sample}$$

Where $area_a = the \ analyte's \ peak \ area \ in \ the \ sample,$ $mass_{istd} = the \ mass \ of \ internal \ standard \ spiked \ into \ the \ sample, \ and$ $area_{istd} = the \ internal \ standard's \ peak \ area \ in \ the \ sample.$

The analyte concentrations are tabulated by Enviroquant and transferred to an Excel spreadsheet.

6.0 Quality Assurance

Each daily analytical batch includes at least one calibration standard, one performance standard, one instrument blank, one procedure blank, and one matrix spike. Acceptance criteria are summarized on the attached Table 3-1. Refer to the IADN Quality Assurance Project Plan (QAPjP) for more details.

7.0 Atrazine

Atrazine is analyzed by GC/MS in the selected ion monitoring mode. The GC temperature program is given in Table 4 below. The calibration standard contains both atrazine and the internal standard d10-anthracene at concentrations of 0.4 ng/ μ L.

The mass spectrometer is turned on after a solvent delay of 8.5 minutes. The ions monitored are m/z 186, m/z 188, m/z 200, and m/z 215. The ions m/z 188 and m/z 200 are the quantitation ions for d10-anthracene and atrazine respectively, and the other two are for confirmation purposes.

Table 4. GC oven temperature program for atrazine analysis.

Initial Temperature: 40°C

Initial Time: 1.00 min

Rate (°C/min)	Final Temperature (°C)	Final Hold Time (min)
25.0	140	0.00
4.0	240	0.00
20.0	290	5.00

Total Run Time: 29.50 min

8.0 Chromatograms

Mass chromatograms from a typical 1 μ L injection of calibration standard are given on the following pages in Figures 1a-i. The windows on the left-hand side of each page show the quantitation peak(s) for one or more PAHs, and those on the right give the corresponding confirmation peaks. Similar mass chromatograms (Figure 2) are given for a 1 μ L injection of the atrazine calibration standard.

Table 5. Calibration standard.

Retention Order	Compound	Concentration (ng/µL)
1	d10-anthracene*	0.20
2	acenaphthylene	0.20
3	acenaphthene	0.20
4	fluorene	0.20
5	phenanthrene	0.20
6	d10-phenanthrene**	0.20
7	anthracene	0.20
8	fluoranthene	0.20
9	pyrene	0.20
10	retene	0.20
11	d12-benzo (a) anthracene*	0.20
12	benzo (a) anthracene	0.20
13	chrysene	0.20
14	d12-perylene*	0.20
15	benzo (b) fluoranthene	0.20
16	benzo (k) fluoranthene	0.20
17	benzo (e) pyrene	0.19
18	benzo (a) pyrene	0.20
19	indeno (1,2,3,cd) pyrene	0.20
20	dibeno (a,h) anthracene	0.20
21	benzo (g,h,i) perylene	0.20
22	coronene	0.20

^{*}internal standard

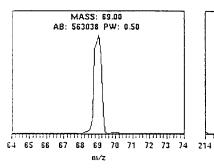
Table 6. SIM windows for analyte detection.

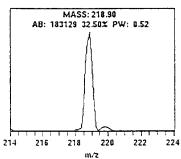
SIM Window	Start Time (min)	SIM Mass (m/z)
1	6.50	76, 83, 151, 152, 153, 154, 165, 166
2	9.80	101, 202, 176, 178, 188, 204, 219, 234
3	11.70	114, 126, 152, 228, 240, 264
4	14.80	138, 139, 150, 276, 278, 279, 300

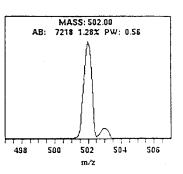
^{**}surrogate standard

Auta Tune Tune File: atune.u Tue Apr 11 95 05:08:05 PM Instrument Name: hp1 Instrument Type: 5989 Ionization Mode: El

Repeller Ion Focus Gain	7.00 255	Multiplier AMU Gain	1583 167	Emission Elec. Energy	300 70	Integration Samples	50 16
lon Focus	34	AMU Offset	106	Polarity	POSITIVE	Averages	1
Entrance Lens	145	nisp cixA	63	Source Temp	250	Stepsize	0.12
Y Rau	4n	Avie Offeet	4	Quad Temp	100	•	







MASS	Abundance	Rel. Abund.	lso. Mass	Iso. Abund.	lso. Ratio
69.00	422528	100.00	70.00	4093	0.97
218.90	158464	37.50	219.90	6279	3.96
501.95	6714	1.59	502.95	672	10.01

Scan: 10.00 - 800.00 samples: 16 thresh: 20 Tue Apr 11 95 05:08:16 PM 259 peaks Base: 69.00 Abundance: 422528

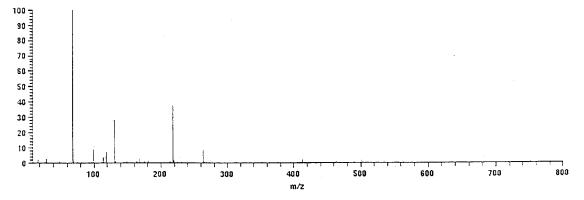


Table 3.1. Data Quality Objectives for Trace Organic Compounds

QA Criteria	QC Code	Sample Type	Frequency	Required Objective	Control Action Un	Units
precision	FD1/ FD2	field; co-located samplers	20%	at <5xMDL, rsd <100% at <5xMDL, rsd <50%	re-analyze if sample available; otherwise flag % samples FFD or PTS	, ₀
	LD1/ LD2	laboratory: replicate analyses	10%	at <5xMDL, rsd <50% at <5xMDL, rsd <30%	re-analyze same or alt sample; otherwise flag % samples FDL or PTS	,o
accuracy	LSS	surrogate spikes	all samples	50% < R <130%	flag PCB congener range FSS; investigate sources % of loss	, 0
	LMS	matrix spikes	1/batch	50% < R < 130% for 70% of individual congeners and for average	flag sample FMS; % investigate sources of loss	\ 0
blanks	FRB	field matrix blank	10% (1/month)	10% (1/month) <20% of associated sample	flag samples FFR; find source of contamination ma	mass
	LRB	lab matrix blank	10%	mass <mdl< td=""><td>run 2nd LRB; elminate source of imprecision; flag mass sample FBS</td><td>nass</td></mdl<>	run 2nd LRB; elminate source of imprecision; flag mass sample FBS	nass
completeness		field samples		%06	no action; % reported	
calibration	CLM	multiple point calibration; 4 point	annual	$ m r^2\!>\!0.95$	reoptimize instrument, repeat calibration	
	CLS	single calibration std	1/10 samples	PCBs ± 10% actual mass	reoptimize instrument, repeat calibration	
	LPC	performance std	daily	see Table 3.2	regenerate response factors	
	LCB	lab calibration blank	2/GC run	< MDL	check for contamination; reoptimize instrument	
PCB identification		GCMS confirmation	2%			
detection limits		MDL study	1/project		reported in yearly QA Report	
detectability	RFS	routine field samples	all samples	> MDL	flag BDL	
holding time	RFS	routine field sample	all samples	l year	flag EHT	

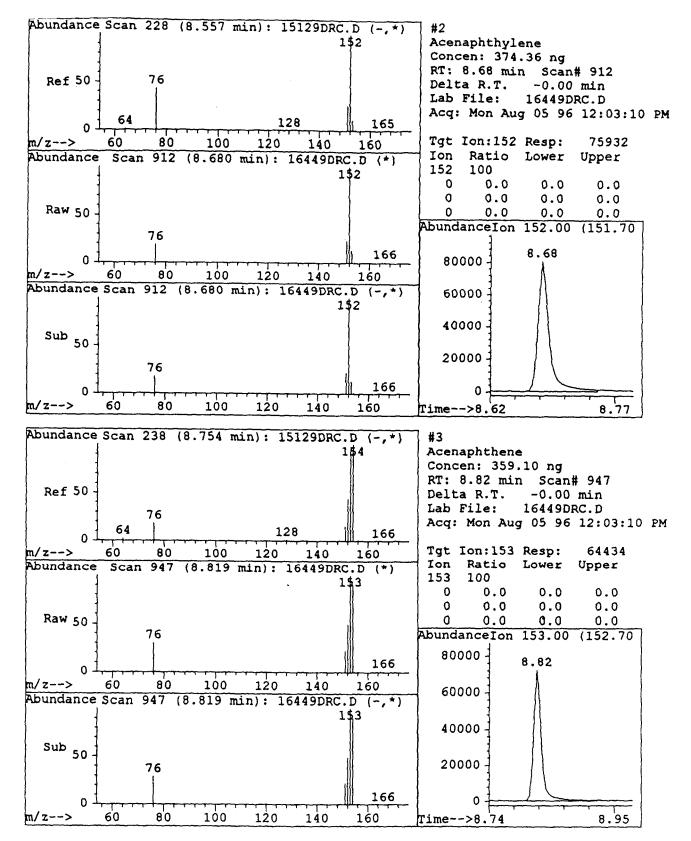


Figure 1a.

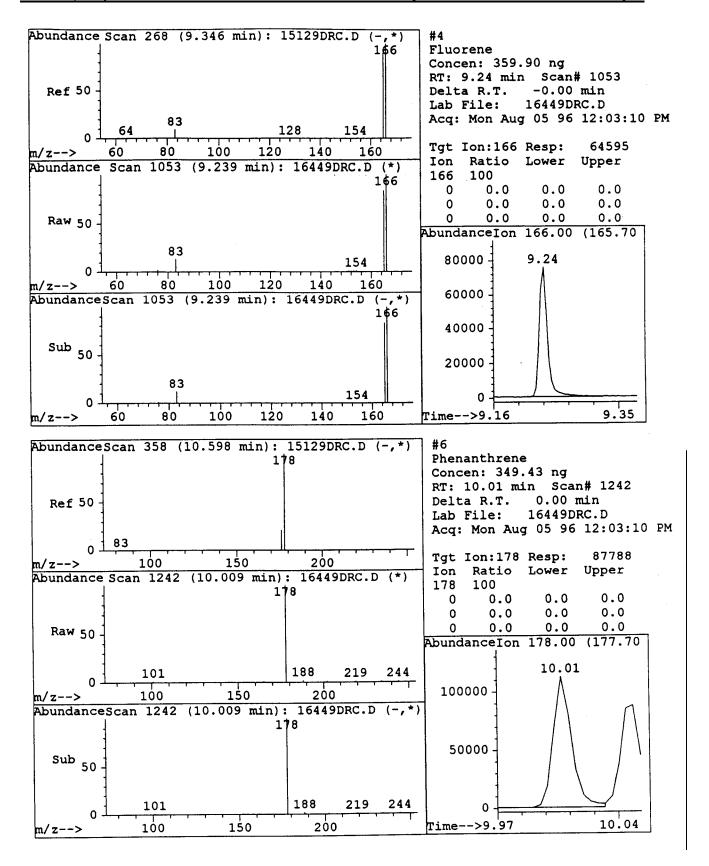


Figure 1b.

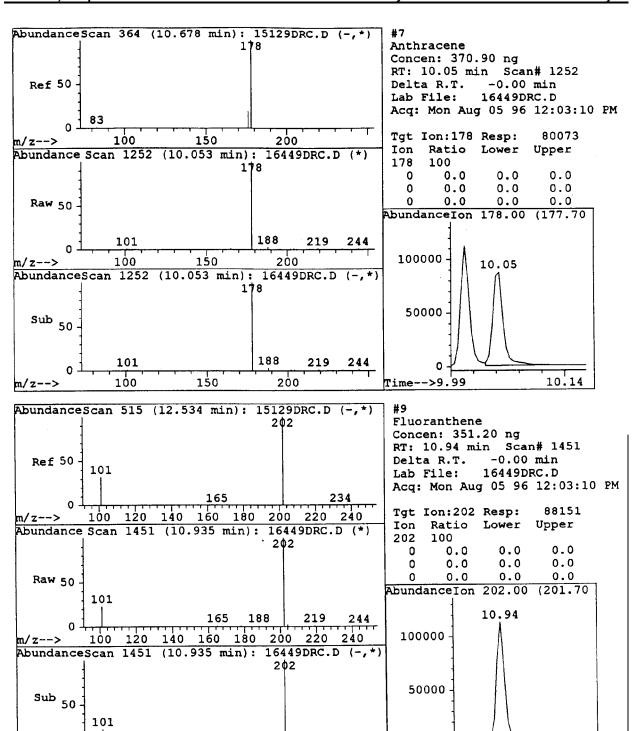


Figure 1c.

219

220

244

240

0

Time-->10.87

11.02

165

120 140 160 180 200

m/z-->

100

188

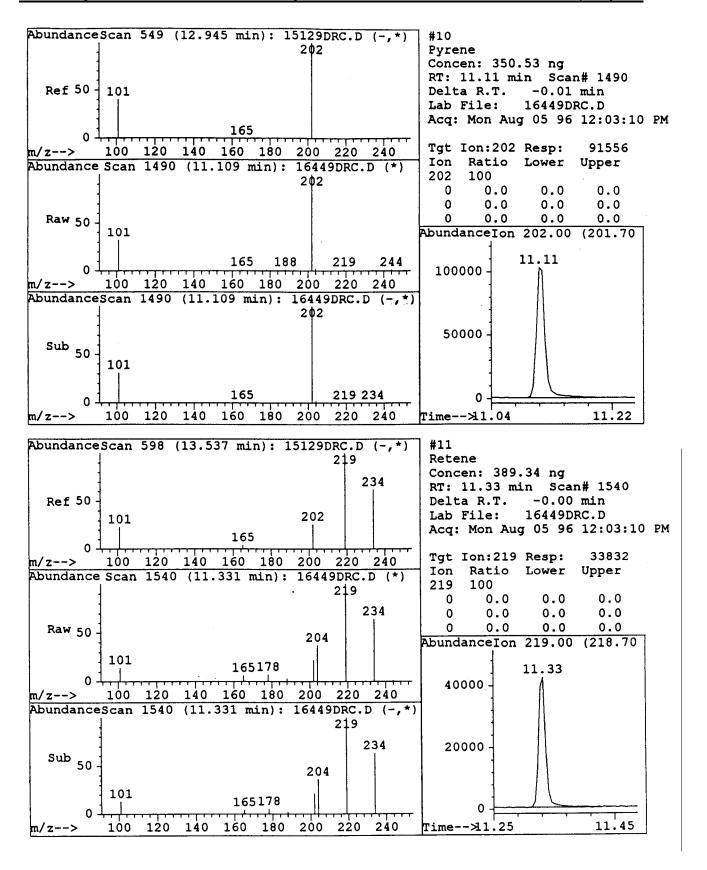


Figure 1d.

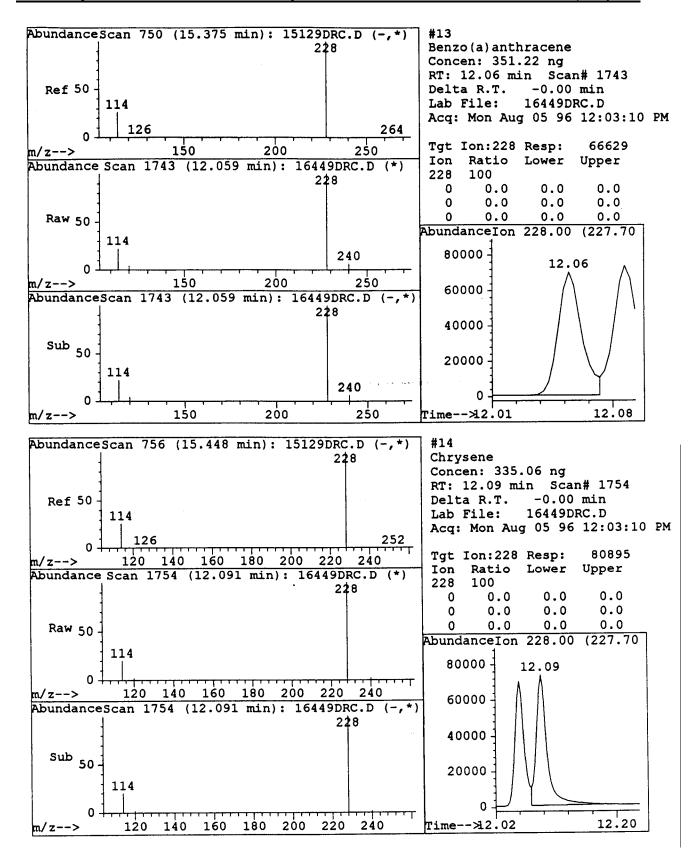


Figure 1e.

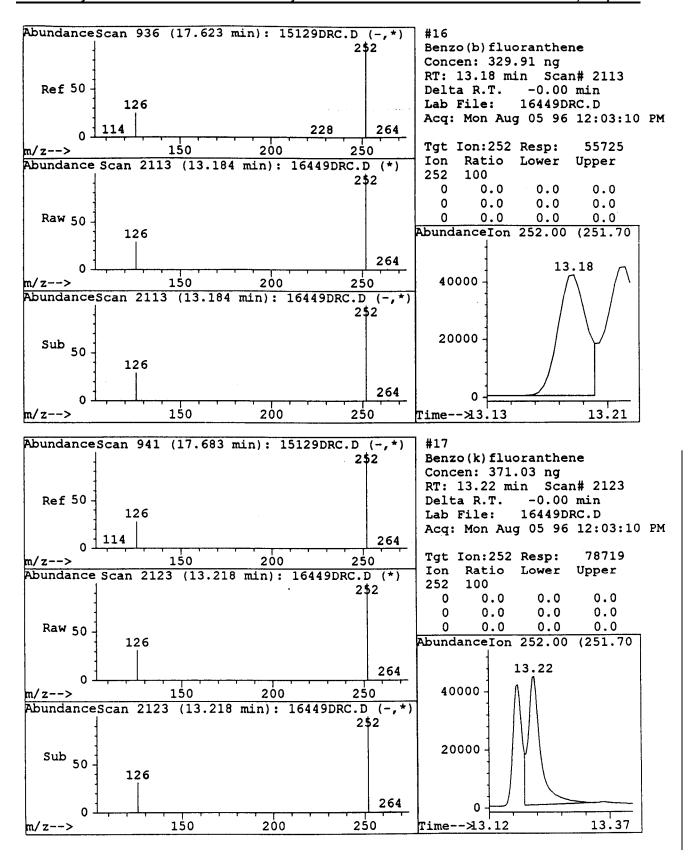


Figure 1f.

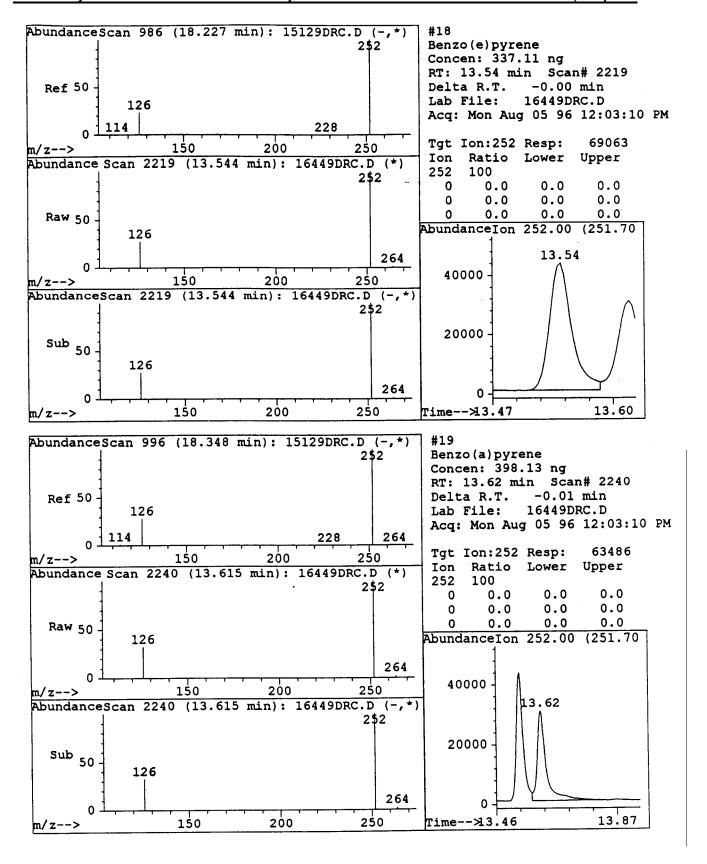


Figure 1g.

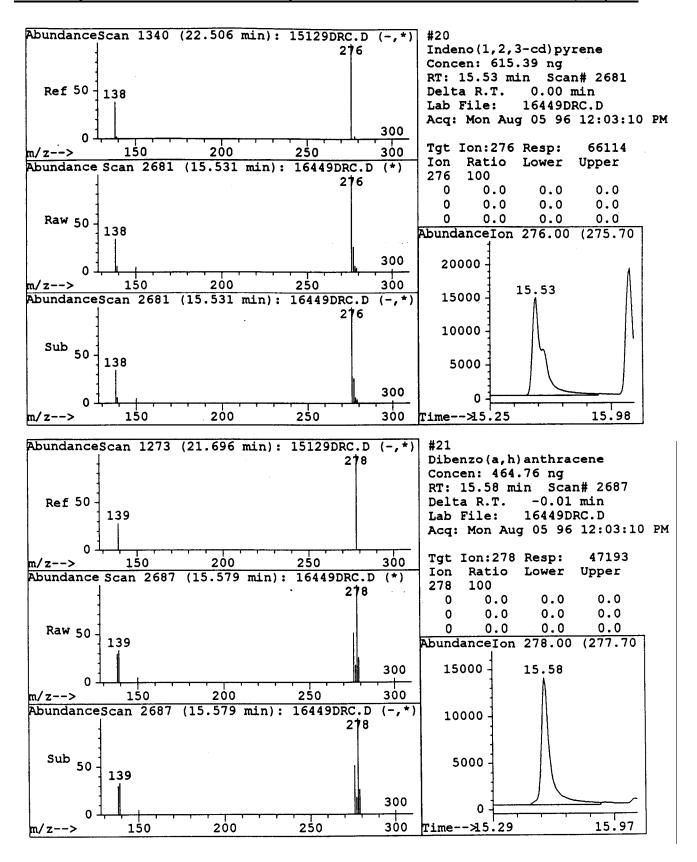


Figure 1h.

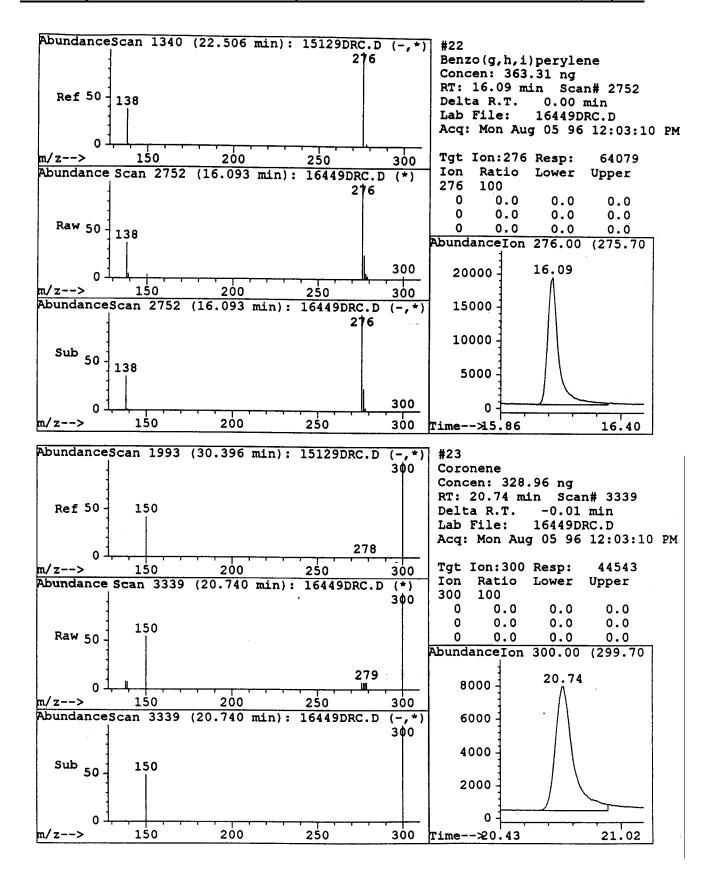


Figure 1i.

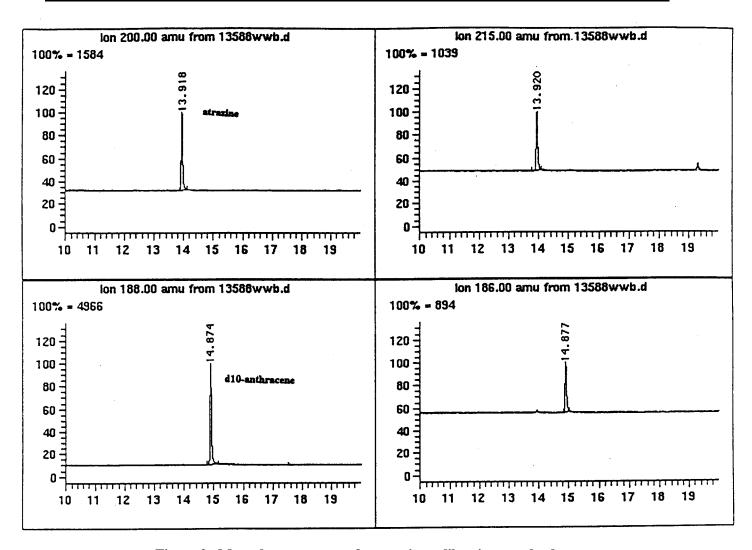


Figure 2. Mass chromatograms for atrazine calibration standard.